Resource Summary Report

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InteroPorc

RRID:SCR_002067
Type: Tool

Proper Citation

InteroPorc (RRID:SCR_002067)

Resource Information

URL: http://biodev.extra.cea.fr/interoporc/

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Description: Automatic prediction tool to infer protein-protein interaction networks, it is applicable for lots of species using orthology and known interactions. The interoPORC method is based on the interolog concept and combines source interaction datasets from public databases as well as clusters of orthologous proteins (PORC) available on Integr8. Users can use this page to ask InteroPorc for all species present in Integr8. Some results are already computed and users can run InteroPorc to investigate any other species. Currently, the following databases are processed and merged (with datetime of the last available public release for each database used): IntAct, MINT, DIP, and Integr8.

Abbreviations: InteroPorc

Synonyms: InteroPorc: Automatic molecular interaction predictions, Automatic molecular interaction predictions

Resource Type: data analysis software, software application, source code, data processing software, data or information resource, analysis service resource, service resource, database, production service resource, data analysis service, software resource

Defining Citation: PMID:18508856

Keywords: orthology, prediction, protein interaction, tool, sequenced genome, proteinprotein interaction, inferred interaction, molecular interaction, interaction, protein, bio.tools

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Marie Curie Fellowship ;
French National Agency of Research ANR Biosys06_134823 SULFIRHOM;

French Atomic Energy Commission

Availability: Open unspecified license, Acknowledgement requested

Resource Name: InteroPorc

Resource ID: SCR_002067

Alternate IDs: nif-0000-20816, biotools:interoporc

Alternate URLs: https://bio.tools/interoporc

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250509T055526+0000

Ratings and Alerts

No rating or validation information has been found for InteroPorc.

No alerts have been found for InteroPorc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Huo T, et al. (2015) Prediction of host - pathogen protein interactions between Mycobacterium tuberculosis and Homo sapiens using sequence motifs. BMC bioinformatics, 16(1), 100.

Basha O, et al. (2015) MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts. Nucleic acids research, 43(W1), W258.

Lv Q, et al. (2015) Genome-wide protein-protein interactions and protein function exploration in cyanobacteria. Scientific reports, 5, 15519.

Pesch R, et al. (2013) Complementing the Eukaryotic Protein Interactome. PloS one, 8(6), e66635.

Trabuco LG, et al. (2012) Negative protein-protein interaction datasets derived from large-scale two-hybrid experiments. Methods (San Diego, Calif.), 58(4), 343.